



PCT

## RAW SEQUENCE LISTING

DATE: 07/14/2004

PATENT APPLICATION: US/10/500,696

TIME: 09:55:49

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\07142004\J500696.raw

1 <110> APPLICANT: ImmuneMed Inc.  
2 KIM, Yoon-Won  
3 KIM, Young-Jin  
4 CHOI, Yo-Han  
5 AHN, Jee-Yin  
6 WOO, Soo-Dong  
7 SIN, Song-Woo  
8 CHO, Min-Kee  
9 BYUN, Young-Hwan  
10 KANG, Jeung-Yul  
12 <120> TITLE OF INVENTION: Novel anti-viral VSF protein and hybridoma producing the  
same  
14 <130> FILE REFERENCE: 7037-69151-01  
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/500,696  
C--> 16 <141> CURRENT FILING DATE: 2004-07-01  
16 <150> PRIOR APPLICATION NUMBER: KR10-2002-0005969  
17 <151> PRIOR FILING DATE: 2002-02-01  
19 <150> PRIOR APPLICATION NUMBER: PCT/KR03/00231  
20 <151> PRIOR FILING DATE: 2003-01-30  
22 <160> NUMBER OF SEQ ID NOS: 74  
24 <170> SOFTWARE: KopatentIn 1.71  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 1401  
28 <212> TYPE: DNA  
29 <213> ORGANISM: mouse  
31 <220> FEATURE:  
32 <221> NAME/KEY: CDS  
33 <222> LOCATION: (1)..(1401)  
34 <223> OTHER INFORMATION: VSF H Protein  
37 <400> SEQUENCE: 1  
38 atg gga tgg agc tgg atc ttt ctc ttc ctt ctg tca gta act gca ggt 48  
39 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Val Thr Ala Gly  
40 1 5 10 15  
42 gtc cac tct gag atc cag ctg cag cag tct gga gct gag ctg gtg aag 96  
43 Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys  
44 20 25 30  
46 cct ggg gct tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttc 144  
47 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe  
48 35 40 45  
50 act ggc tac aac atg aac tgg gtg aag cag agc cat gga aag agc ctt 192  
51 Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu  
52 50 55 60  
54 gag tgg att gga aat att gat cct tac tat ggt agt act acc tac aat 240  
55 Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Ser Thr Thr Tyr Asn



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56	65	70	75	80	
58	cag aag ttc aag ggc aag gcc aca ttg act gta gac aaa tct tcc agc	288			
59	Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser				
60	85 90 95				
62	aca gcc tac atg cag ctc aac agc ctg aca tct gag gac tct gca gtc	336			
63	Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val				
64	100 105 110				
66	tat tac tgt gca aga gag act ggg acg agg gct atg gac tac tgg ggt	384			
67	Tyr Tyr Cys Ala Arg Glu Thr Gly Thr Arg Ala Met Asp Tyr Trp Gly				
68	115 120 125				
70	caa gga acc tca gtc acc gtc tcc tca gct aca aca aca gcc cca tct	432			
71	Gln Gly Thr Ser Val Thr Val Ser Ser Ala Thr Thr Thr Ala Pro Ser				
72	130 135 140				
74	gtc tat ccc ttg gtc cct ggc tgc agt gac aca tct gga tcc tcg gtg	480			
75	Val Tyr Pro Leu Val Pro Gly Cys Ser Asp Thr Ser Gly Ser Ser Val				
76	145 150 155 160				
78	aca ctg gga tgc ctt gtc aaa ggc tac ttc cct gag ccg gta act gta	528			
79	Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val				
80	165 170 175				
82	aaa tgg aac tat gga gcc ctg tcc agc ggt gtg cgc aca gtc tca tct	576			
83	Lys Trp Asn Tyr Gly Ala Leu Ser Ser Gly Val Arg Thr Val Ser Ser				
84	180 185 190				
86	gtc ctg cag tct ggg ttc tat tcc ctc agc agc ttg gtg act gta ccc	624			
87	Val Leu Gln Ser Gly Phe Tyr Ser Leu Ser Ser Leu Val Thr Val Pro				
88	195 200 205				
90	tcc agc acc tgg ccc agc cag act gtc atc tgc aac gta gcc cac cca	672			
91	Ser Ser Thr Trp Pro Ser Gln Thr Val Ile Cys Asn Val Ala His Pro				
92	210 215 220				
94	gcc agc aag act gag ttg atc aag aga atc gag cct aga ata ccc aag	720			
95	Ala Ser Lys Thr Glu Leu Ile Lys Arg Ile Glu Pro Arg Ile Pro Lys				
96	225 230 235 240				
98	ccc agt acc ccc cca ggt tct tca tgc cca cct ggt aac atc ttg ggt	768			
99	Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro Gly Asn Ile Leu Gly				
100	245 250 255				
102	gga cca tcc gtc ttc atc ttc ccc cca aag ccc aag gat gca ctc atg	816			
103	Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ala Leu Met				
104	260 265 270				
106	atc tcc cta acc ccc aag gtt acg tgt gtg gtg gtg gat gtg agc gag	864			
107	Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Val Ser Glu				
108	275 280 285				
110	gat gac cca gat gtc cat gtc agc tgg ttt gtg gac aac aaa gaa gta	912			
111	Asp Asp Pro Asp Val His Val Ser Trp Phe Val Asp Asn Lys Glu Val				
112	290 295 300				
114	cac aca gcc tgg aca cag ccc cgt gaa gct cag tac aac agt acc ttc	960			
115	His Thr Ala Trp Thr Gln Pro Arg Glu Ala Gln Tyr Asn Ser Thr Phe				
116	305 310 315 320				
118	cga gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agg ggc	1008			
119	Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Arg Gly				
120	325 330 335				

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122 aag gag ttc aaa tgc aag gtc aac aac aaa gcc ctc cca gcc ccc atc      1056
123 Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile
124          340          345          350
126 gag aga acc atc tca aaa ccc aaa gga aga gcc cag aca cct caa gta      1104
127 Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg Ala Gln Thr Pro Gln Val
128          355          360          365
130 tac acc ata ccc cca cct cgt gaa caa atg tcc aag aag aag gtt agt      1152
131 Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met Ser Lys Lys Lys Val Ser
132          370          375          380
134 ctg acc tgc ctg gtc acc aac ttc ttc tct gaa gcc atc agt gtg gag      1200
135 Leu Thr Cys Leu Val Thr Asn Phe Phe Ser Glu Ala Ile Ser Val Glu
136 385          390          395          400
138 tgg gaa agg aac gga gaa ctg gag cag gat tac aag aac act cca ccc      1248
139 Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp Tyr Lys Asn Thr Pro Pro
140          405          410          415
142 atc ctg gac tca gat ggg acc tac ttc ctc tac agc aag ctc act gtg      1296
143 Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Thr Val
144          420          425          430
146 gat aca gac agt tgg ttg caa gga gaa att ttt acc tgc tcc gtg gtg      1344
147 Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile Phe Thr Cys Ser Val Val
148          435          440          445
150 cat gag gct ctc cat aac cac cac aca cag aag aac ctg tct cgc tcc      1392
151 His Glu Ala Leu His Asn His His Thr Gln Lys Asn Leu Ser Arg Ser
152          450          455          460
154 cct ggt aaa      1401
155 Pro Gly Lys
156 465
159 <210> SEQ ID NO: 2
160 <211> LENGTH: 467
161 <212> TYPE: PRT
162 <213> ORGANISM: mouse
164 <400> SEQUENCE: 2
165 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
166 1          5          10          15
168 Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
169          20          25          30
171 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
172          35          40          45
174 Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu
175          50          55          60
177 Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Ser Thr Thr Tyr Asn
178 65          70          75          80
180 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
181          85          90          95
183 Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
184          100          105          110
186 Tyr Tyr Cys Ala Arg Glu Thr Gly Thr Arg Ala Met Asp Tyr Trp Gly
187          115          120          125
189 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Thr Thr Thr Ala Pro Ser

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```

190      130      135      140
192 Val Tyr Pro Leu Val Pro Gly Cys Ser Asp Thr Ser Gly Ser Ser Val
193 145      150      155      160
195 Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
196      165      170      175
198 Lys Trp Asn Tyr Gly Ala Leu Ser Ser Gly Val Arg Thr Val Ser Ser
199      180      185      190
201 Val Leu Gln Ser Gly Phe Tyr Ser Leu Ser Ser Leu Val Thr Val Pro
202      195      200      205
204 Ser Ser Thr Trp Pro Ser Gln Thr Val Ile Cys Asn Val Ala His Pro
205      210      215      220
207 Ala Ser Lys Thr Glu Leu Ile Lys Arg Ile Glu Pro Arg Ile Pro Lys
208 225      230      235      240
210 Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro Gly Asn Ile Leu Gly
211      245      250      255
213 Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ala Leu Met
214      260      265      270
216 Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Val Ser Glu
217      275      280      285
219 Asp Asp Pro Asp Val His Val Ser Trp Phe Val Asp Asn Lys Glu Val
220      290      295      300
222 His Thr Ala Trp Thr Gln Pro Arg Glu Ala Gln Tyr Asn Ser Thr Phe
223 305      310      315      320
225 Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Arg Gly
226      325      330      335
228 Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile
229      340      345      350
231 Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg Ala Gln Thr Pro Gln Val
232      355      360      365
234 Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met Ser Lys Lys Lys Val Ser
235      370      375      380
237 Leu Thr Cys Leu Val Thr Asn Phe Phe Ser Glu Ala Ile Ser Val Glu
238 385      390      395      400
240 Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp Tyr Lys Asn Thr Pro Pro
241      405      410      415
243 Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Thr Val
244      420      425      430
246 Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile Phe Thr Cys Ser Val Val
247      435      440      445
249 His Glu Ala Leu His Asn His His Thr Gln Lys Asn Leu Ser Arg Ser
250      450      455      460
252 Pro Gly Lys
253 465
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 702
258 <212> TYPE: DNA
259 <213> ORGANISM: mouse
261 <220> FEATURE:
262 <221> NAME/KEY: CDS

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263 <222> LOCATION: (1)..(702)
264 <223> OTHER INFORMATION: VSF L3 Protein
267 <400> SEQUENCE: 3
268 atg agt gtg ccc act cag gtc ctg ggg ttg ctg ctg ctg tgg ctt aca      48
269 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
270   1           5           10          15
272 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct      96
273 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
274           20           25           30
276 gca tct gtg gga gaa act gtc acc atg aca tgt cga gca agt gag aat      144
277 Ala Ser Val Gly Glu Thr Val Thr Met Thr Cys Arg Ala Ser Glu Asn
278           35           40           45
280 att tac agt aat tta gca tgg tat cag cag aaa cag gga aaa tct cct      192
281 Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
282   50           55           60
284 cag ctc ctg gtc tat gtt gca aca aac tta gca gat ggt gtg cca tca      240
285 Gln Leu Leu Val Tyr Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
286  65           70           75           80
288 agg ttc agt ggc agt gga tca ggc aca cag ttt tct ctg aag atc aac      288
289 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
290           85           90           95
292 agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tat      336
293 Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Tyr
294           100          105          110
296 ggt tct cct cgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg      384
297 Gly Ser Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
298           115          120          125
300 gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag cag      432
301 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
302           130          135          140
304 tta aca tct gga ggt gcc tca gtc gtg tgc ttc ttg aac aac ttc tac      480
305 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
306 145          150          155          160
308 ccc aga gac atc aat gtc aag tgg aag att gat ggc agt gaa cga caa      528
309 Pro Arg Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
310           165          170          175
312 aat ggt gtc ctg aac agt tgg act gat cag gac agc aaa gac agc acc      576
313 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
314           180          185          190
316 tac agc atg agc agc acc ctc aca ttg acc aag gac gag tat gaa cga      624
317 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
318           195          200          205
320 cat aac aac tat acc tgt gag gcc act cac aag aca tca act tca ccc      672
321 His Asn Asn Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
322           210          215          220
324 atc gtc aag agc ttc aac agg aat gag tgt      702
325 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
326 225          230
329 <210> SEQ ID NO: 4

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/500,696

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\07142004\J500696.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date